

FIG 1

1 CCG CTC ACA TTG CGA TTC GTC ATT CTT CTT CTA AAA CCC GCA AAA TTT CTC CAT TTC TAC
 61 CAA AAA TAT CCA ACT TTT ACT TTT CTT TCC TGT GAA ATT ATC TGC TCA AAT CTT TGG TTC
 121 CTG ACG GAG ATG GCG GCG ATT TCA GGC ATC TCC TCT GGT ACG TIG ACG ATT TCA CGG CCT
 M A A I S G I S S G T L T I S R P
 181 TTG GTT ACT CTT CGA CGC TCT AGA GCC GCC GTT TCG TAC AGC TCC TCT CAC CGA TTG CTT
 L V T L R R S R A A V S Y S S S H R L L
 241 CAT CAT CTT CCT CTC TCT CGT CGT CTG CTA TTA AGG AAC AAT CAT CGA GTC CAA GCA
 H H L P L S S R R L L R N N H R V O * A
 301 ACG ATT TTG CAA GAC GAT GAA GAG AAA GTG CTG GTG GAG GAA TCG TTT AAA GCC GAG ACT
 T I L Q D D E E K V V V E E S F K A E T
 361 TCT ACT GGT ACA GAA CCA CTT GAG GAG CCA AAT ATG AGT TCT TCT TCA ACT AGT GCT TTT
 S T G T E P L E E P N M S S S S T S A F
 421 GAG ACA TGG ATC ATC AAG CTT GAG CAA GGA GTG AAT GTT TTC CTT ACA GAC TCG GTT ATT
 E T W I I K L E Q G V N V F L T D S V I
 481 AAG ATA CTT GAC ACT TTG TAT CGT GAC CGA ACA TAT GCA AGG TTC TTT GTT CTT GAG ACA
 K I L D T L Y R D R T Y A R F F V L E T
 541 ATT CCT AGA GTG CCT TAT TTT GCG TTT ATG TCT GTG CTA CAT ATG TAT GAG ACC TTT GGT
 I A R V P Y F A F M S V L H M Y E T F G
 601 TGG TGG AGG AGA GCA GAT TAT TTG AAA GTA CAC TTT GCT GAG AGC TGG AAT GAA ATG CAT
 W W R R A D Y L K V H F A E S W N E M H
 661 CAC TTG CTC ATA ATG GAA GAA TTG GGT GGA AAT TCT TGG TGG TTT GAT CGT TTT CTG GCT
 H L L I M E E L G G N S W W F D R F L A
 721 CAG CAC ATA GCA ACC TTC TAC TAC TTC ATG ACA GTG TTC TTG TAT ATC TTA ACC CCT AGA
 Q H I A T F Y Y F M T V F L Y I L S P R
 781 ATG GCA TAT CAC TTT TCG GAA TGT GTG GAG AGT CAT GCA TAT GAG ACT TAT GAT AAA TTT
 M A Y H F S E C V E S H A Y E T Y D K F
 841 CTC AAG GCC AGT GGA GAG GAG TTG AAG AAT ATG CCT GCA CCG GAT ATC GCA GCA AAA TAC
 L K A S G E E L K N M P A P D I A V K Y
 901 TAT ACG GGA GGT GAC TTG TAC TTA TTT GAT GAG TTC CAA ACA TCA AGA ACT CCC AAT ACT
 Y T G G D L Y L F D E F Q T S R T P N T
 961 CGA AGA CCA GCA ATA GAA AAT CTA TAC GAT GTG TTT GTG AAC ATA AGA GAT GAT GAA GCA
 R R P V I E N L Y D V F V N I R D D E A
 1021 GAA CAC TGC AAG ACA ATG AGA GCT TGT CAG ACT CTA GGC AGT CTG CGT TCT CCA CAC TCC
 E H C K T M R A C Q T L G S L R S P H S
 1081 ATT TTA GAT GAT GAT ACT GAA GAA GAA TCA GGG TGT GTT GTT CCT GAG GAG GCT CAT
 I L D D D T E E E S G C V V P E E A H
 1141 TGC GAA GGT ATT GTA GAC TGC CTC AAG AAA TCC ATT ACA AGT TAA TAA ATT AGA AAG TAA
 C E G I V D C L K K S I T S
 1201 ACT AAA AAA GAT TAT TTG TAT CAG CTC ATG AAC AAT AGA TAT AAT CCC ATA TAC TTG GGA
 1261 ATA AAG GAA TAA TGT GAA ATT CCC ATC GTT GTG CTA GTG TGT GAG AGA ATC AAA TAC CCT
 1321 AAT GAT GTA AAT GTA CTT TGA TGA GCT TAA GTC GTT GTA GAC CAT TTT ATC AAA AAA AAA
 1381 AAA AAA AAA AAA AAA A

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FIG 2

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FIG 3

T 1 MAISISAMSFGTSVSSYSCFRARSFEKSSVLCNSQNPCRFNSVFP. IRKSDGASRCVSRR

P 1 MAISISAMSFRTSVSS.....SY..SAFLCNSKNPFCLNSLFS.LRNSHRTFQPSLSR

A 1 MA.AISGISSGTLTIS.....RPLVTLRRSRAAVSYSSSHRLLLHHLPLSSRRLLL
consensus

1 MA ISamS T S L S S 1r 1 R

T 60 KSCRVRATLLQENEVEEVVVEKSFAPKSFPDNVGGSNGKPPDDSSS.NGLEKWWVIKLEQS

P 51 KSSRVRATLLKENEEEVVVEKSFAPKSFPGNVGGSNGEPPDNESSS.NGLEKWWVIKIEQS

A 51 NNHRVQATILQDDEEKVVVEESFKAETSTGTPELEPNMSSSTSFAETWIICKLEQG
consensus

61 RV AT1L e EE VVVE SF G P SSS g E WvIKieQ

T 119 VNILLTDSVIKILDLYHNRNYARFFVLETIARVPYFAFISVLHMYESFGWWRRADYMKV

P 110 VNIFLTDSVIKILDLYHDRHYARFFVLETIARVPYFAFISVLHLYESFGWWRRADYLKV

A 108 VNVFLTDSVIKILDLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWWRRADYLKV
consensus

121 VNI LTDSVIKILDLYh R YARFFVLETIARVPYFAFISVLHLYEesFGWWRRADY1KV

T 179 HFAESWNEMHHLLIMEELGGNAWWFDRFLAQHIAIFYYFMTVLMYALSPRMAYHFSECVE

P 170 HFAESWNEMHHLLIMEELGGNAWWFDRFLAQHIAVFYYFMTVSMYALSPRMAYHFSECVE

A 168 HFAESWNEMHHLLIMEELGGNSWFDRFLAQHIATFYFMTVFLYILSPRMAYHFSECVE
Consensus

181 HFAESWNEMHHLLIMEELGGN WWFDRFLAQHIA FYYFMTV mY LSPRMAYHFSECVE

T 239 SHAYETYDKFIKDQGEELKNLPAPKIAVDYYTGGDLYLFDDEFQTSREPNTRRPIDNLYD

P 230 HHAYETYDKFIKDQEAEKKLPAPKIAVSYYTGGDLYLFDDEFQTSREPNTRRPIDNLYD

A 227 SHAYETYDKFLKASGEELKNMPAPDIAVKYYTGGDLYLFDDEFQTSRTPNTRRPVIENLYD
Consensus

241 HAYETYDKFIK ELK 1PAP IAV YYTGGDLYLFDDEFQTSR PNTRRP IdNLYD

T 299 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTD.PCDDSEDDTGCSVQ.QADCIGIVDCIKK

P 290 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTN.PCDESEDDPGCSVQ.QADCVGIVDCITK

A 287 VFVNIRDDEAEHCKTMRACQTLGSLRSPHSILDDDDTEEESGCVVPEEAHCEGIVDCLKK
Consensus

301 VFmNIRDDEAEHCKTMkACQT GSLRSPHt DdeEdd GC VP A C GIVDCi K

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FIG 3 (suite)

T 357 SVTDTQVTKR

P 348 SVADPNVGRR

A 347 SITS.....

Consensus

361 Sv

FIG 4

FIG 4A

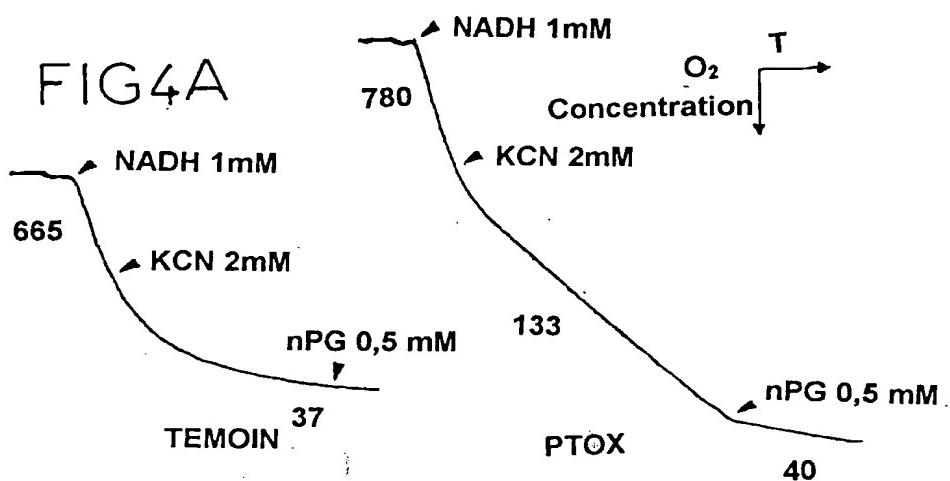


FIG 4B

